

New archaeal methyltransferases forming 1-methyladenosine or 1-methyladenosine and 1-methylguanosine at position 9 of tRNA

Morgane Kempenaers¹, Martine Roovers², Yamina Oudjama², Karolina L. Tkaczuk^{3,4}, Janusz M. Bujnicki^{3,5} and Louis Droogmans^{1,*}

¹Laboratoire de Microbiologie, Université Libre de Bruxelles (ULB), ²Institut de Recherches Microbiologiques Jean-Marie Wiame, Avenue E. Gryson 1, B-1070 Bruxelles, Belgium, ³International Institute of Molecular and Cell Biology in Warsaw, Trojdena 4 St., PL-02-109 Warsaw, ⁴Institute of Technical Biochemistry, Technical University of Lodz, B. Stefanowskiego 4/10, PL-90-924 Lodz and ⁵Institute of Molecular Biology and Biotechnology, Faculty of Biology, Adam Mickiewicz University, PL-61-614 Poznan, Poland

Received February 22, 2010; Revised May 9, 2010; Accepted May 10, 2010

ABSTRACT

Two archaeal tRNA methyltransferases belonging to the SPOUT superfamily and displaying unexpected activities are identified. These enzymes are orthologous to the yeast Trm10p methyltransferase, which catalyses the formation of 1-methylguanosine at position 9 of tRNA. In contrast, the Trm10p orthologue from the crenarchaeon *Sulfolobus acidocaldarius* forms 1-methyladenosine at the same position. Even more surprisingly, the Trm10p orthologue from the euryarchaeon *Thermococcus kodakaraensis* methylates the N¹-atom of either adenosine or guanosine at position 9 in different tRNAs. This is to our knowledge the first example of a tRNA methyltransferase with a broadened nucleoside recognition capability. The evolution of tRNA methyltransferases methylating the N¹ atom of a purine residue is discussed.

INTRODUCTION

Cellular RNAs possess numerous chemically modified nucleosides, but the largest number and the greatest variety are found in transfer RNA (tRNA). These modifications are introduced by many different enzymes during the complex process of RNA maturation. The functions of these modified nucleosides are not well known, but it seems that modifications in the anticodon region play a direct role in increasing translational efficiency and fidelity, while modifications outside the anticodon region

are typically involved in the maintenance of the structural integrity of tRNA. Among naturally occurring nucleoside modifications, base and ribose methylations are by far the most frequently encountered (1,2). These methylations are catalysed by tRNA methyltransferases (MTases) that use S-adenosyl-L-methionine (AdoMet) as the methyl donor, with a single exception of a recently identified enzyme, which uses a folate as the methyl donor (3).

AdoMet-dependent MTases belong to at least seven evolutionarily and structurally unrelated classes/superfamilies (4–6). Most of the known RNA MTases belong to class I. They possess a fold similar to the Rossmann fold, and are therefore called Rossmann fold MTases (RFM). The structure comprises a seven-stranded β sheet with a central topological switch-point and a characteristic reversed β hairpin at the carboxyl end of the sheet (6 \uparrow 7 \downarrow 5 \uparrow 4 \uparrow 1 \uparrow 2 \uparrow 3 \uparrow). This β sheet is flanked by α helices to form an $\alpha\beta\alpha$ sandwich (4). RFM enzymes are typically monomeric although di-tri- or tetrameric structures have been reported. Class IV MTases, also named the SPOUT class MTases, a nomenclature coming from the first two members of this class, SpoU and TrmD, act also on RNA, but are structurally different from the class I MTases (7). They possess a five-stranded β sheet core (5 \uparrow 3 \uparrow 4 \uparrow 1 \uparrow 2 \uparrow) flanked by seven α helices. The most characteristic feature of these enzymes is the presence of a deep topological knot in the C-terminal part of the sheet. This knot is responsible for AdoMet binding. All known SPOUT MTases are dimers, with the catalytic site formed at the interface of two monomers (8).

There are only a few archaeal tRNA specific MTases functionally characterised to date. Those MTases can be

*To whom correspondence should be addressed. Tel: +32 2 526 7275; Fax: +32 2 526 7273; Email: ldroogma@ulb.ac.be
Present address:

Karolina L. Tkaczuk, Department of Molecular Physiology and Biological Physics, University of Virginia, 1300 Jefferson Park Avenue, Charlottesville, VA 22908, USA.

very different in terms of structure, of target or in their mechanism. Some act as base MTases, while others are ribose MTases. Among the MTases acting on ribose, there exist two kinds of methylation pathways. In the first one, called 'all-protein enzyme', the MTase recognizes on its own the target nucleoside and catalyses the methyl transfer on the ribose. The second mechanism involves an MTase taking part of a ribonucleoprotein (RNP) complex, in which the recognition of the target nucleoside is carried out by a small guide RNA. In different organisms, the same modification can be accomplished by the two different mechanisms. This is the case of the Cm56 ribose methylation of tRNA in Archaea. In *Pyrobaculum aerophilum*, this modification is catalysed by a RNP complex, where the small RNA sR35 targets the C56 nucleoside for modification by a protein catalytic subunit, a member of the RFM superfamily (9). This case is an exception in Archaea, because all other archaeal genomes sequenced to date possess a SPOUT MTase homologous to aTrm56 from *Pyrococcus abyssi*, which catalyses non-guided methylation of C56 (9,10).

The six archaeal RFM MTases characterised to date act on the base of nucleosides. Trm-G10 from *P. abyssi* methylates or dimethylates guanosine 10 from tRNA to form m²G10 or m₂G10 (11,12). The same modification can be found at position 26 of tRNA and is catalysed by Trm-G26 (also known as Trm1) (13,14). The MTase encoded by the open reading frame (ORF) PAB1947 from *P. abyssi* acts on several cytosines in tRNA to form m⁵C, with a preference for C49. The specificity of this MTase for C49 is increased by an archaease (15). Another important tRNA MTase identified in Archaea is Trm5, which methylates G37 in tRNA (16). Guanosine in position 37 is commonly methylated to form m¹G37 in tRNA from organisms belonging to the three domains of life, and this modification prevents frame-shifting by assuring correct codon-anticodon pairing (17). The tRNA MTase TrmU54 catalyses the methylation of atom C⁵ in uridine to form ribothymidine in tRNA from *P. abyssi* (18). This modification is invariably found at position 54 in the TΨC loop of tRNAs of most organisms. And finally, the MTase TrmI from *P. abyssi* catalyses the methylation of position N¹ of adenosine to form m¹A. This enzyme displays region specificity, methylating A58 and A57 from TΨC loop of tRNA, m¹A57 being the obligatory intermediate in the biosynthesis of 1-methylinosine (m¹I) (19).

Until now, only one tRNA from hyperthermophilic archaea has been fully sequenced, the initiator methionine tRNA from the crenarchaeon *Sulfolobus acidocaldarius* (20). This tRNA contains 10 modified nucleosides, 9 of them bearing a methylation either on the base or on the ribose, or even both on base and ribose. However, the nature of the modified nucleoside at position 9 is unknown. In yeast, some tRNAs with a guanosine at this position are methylated by the Trm10p MTase, to form m¹G9 (21). As a protein distantly related to the yeast enzyme is encoded by the Saci_1677 gene of *S. acidocaldarius*, it could be a potential candidate for the modification at position 9 of *S. acidocaldarius* tRNA_{Met}.

In this article, we show that the *S. acidocaldarius* Saci_1677p enzyme indeed acts at position 9 of tRNA, catalysing m¹A formation. Furthermore, in Euryarchaeota, the homologous protein from *Thermococcus kodakaraensis* also acts at position 9 of tRNA, but catalyses both m¹A and m¹G formation. To our knowledge, this is the first MTase found to methylate the two purine bases at the same position.

MATERIALS AND METHODS

Strains, media, growth conditions and general procedures

Pwo DNA polymerase, T4 DNA ligase, T7 RNA polymerase, and T4 polynucleotide kinase were purchased from Roche. Ribonuclease A was from Fermentas. Genomic DNA from *T. kodakaraensis* was a gift from H. Grosjean (CNRS, France) and T.J. Santangelo (Ohio State University, USA). Genomic DNA from *S. acidocaldarius* was a gift from D. Charlier (VUB, Belgium). The *S. cerevisiae* Trm10-GST clone plasmid (pYCG_YOL93w) and *S. cerevisiae* Y16243 strain (BY4742; *MATα*; *his3Δ1*; *leu2Δ0*; *lys2Δ0*; *ura3Δ0*; *yol093w::kanMX4*) were purchased from Euroscarf.

Cloning of the *T. kodakaraensis* TK0422 ORF, *S. acidocaldarius* Saci_1677 ORF and of *S. cerevisiae* TRM10 ORF

The TK0422 ORF was amplified from *T. kodakaraensis* genomic DNA using Pwo polymerase (Roche) and the primers TKF (5'-CTAGCATATGAAGACCCTCGCAGATG-3') and TKR (5'-CTAGCTCGAGTCAGCAGTTGTAGCAGAGC-3') containing the NdeI and XhoI restriction sites, respectively. After cloning the PCR product in pCR-Blunt vector (Zero Blunt, Invitrogen), the NdeI/XhoI fragment was extracted and cloned in pET-28b expression vector (Novagen), generating the pTK1 plasmid, allowing expression of an N-terminal His-tagged *T. kodakaraensis* protein in *Escherichia coli*. The Saci_1677 ORF was amplified from *S. acidocaldarius* genomic DNA using Pwo polymerase (Roche) and the primers SAF (5'-CTAGCATATGACACTTGCAAAGGTTTTTCGC-3') and SAR (5'-CTAGCTCGAGTCAA TTTTTTCCCAGTCTAC-3') containing the NdeI and XhoI restriction sites, respectively. After cloning the PCR product in pJET1.2/blunt cloning vector (CloneJET™ Fermentas), the NdeI/XhoI fragment was extracted and cloned in pET-28b expression vector, generating the pSA1 plasmid, allowing expression of an N-terminal His-tagged *S. acidocaldarius* protein in *E. coli*. The TRM10 ORF was amplified from the Trm10-GST clone using Pwo polymerase (Roche) and the primers SCF (5'-CTACATATGTCCAATGATGAGATAAAC C-3') and SCR (5'-CTACTCGAGTGTGTCCTTTGGA GCTGG-3') containing the NdeI and XhoI restriction sites, respectively. After cloning the PCR product in pJET1.2/blunt cloning vector, the NdeI/XhoI fragment was extracted and cloned in pET-28b expression vector, generating the pSC1 plasmid, allowing expression of an N-terminal His-tagged *S. cerevisiae* protein in *E. coli*. The sequences of all clones were checked.

Expression and purification of the recombinant *T. kodakaraensis* TK0422p, *S. acidocaldarius* Saci_1677p and *S. cerevisiae* Trm10p

The His-tagged TK0422p, Saci_1677p and Trm10p recombinant proteins were expressed in *E. coli* strain Rosetta (DE3) (Novagen) carrying extra copies of tRNA genes (*argU*, *argW*, *ileX*, *glyT*, *leuW*, *proL*, *metT*, *thrT*, *tyrU* and *thrU*) specific for rare *E. coli* codons, to aid this expression. Freshly transformed cells were grown to an OD₆₆₀ of 0.5–0.6 at 37°C in 1 l of Luria broth with kanamycin (30 µg/ml). Isopropyl-β-D-thiogalactopyranoside (IPTG) (Roche Diagnostics) was then added to a final concentration of 1 mM to induce recombinant protein expression. Cells were harvested after 3 h incubation at 37°C and resuspended in 100 ml of buffer A (Tris-HCl 50 mM pH 8, KCl 500 mM) complemented with protease inhibitors (Complete, EDTA-free protease inhibitor; Roche Diagnostics) prior to cell disruption by sonication. The lysate was cleared by centrifugation (20 000g for 30 min), and was applied to a Chelating-Sepharose fast flow column (GE Healthcare) charged with Ni²⁺ and equilibrated with buffer A. The column was washed with the same buffer, and the adsorbed material was eluted with a linear gradient (210 ml, from 0 to 1.0 M) of imidazole in buffer A. The fractions containing TK0422p, Saci_1677p and Trm10p were separately pooled. The purified proteins were then submitted to a gel filtration chromatography (Superdex G200; GE Healthcare), leading to almost completely pure TK0422p, Saci_1677p and Trm10p.

T7 *in vitro* transcription of tRNA genes

The general procedure for generating *in vitro* transcripts of tRNA genes is based on the method described previously (22). The sequence of the DNA product obtained after amplification of *S. acidocaldarius* genomic DNA with oligonucleotides MK1 (5'-TCTGCGTAATACGACTC ACTATAGGCGGCGTAGGGAAGCCTGGTATCC C-3') and MK2 (5'-TCTGCGCTGCAGTGGTGGCGGC GCCTGGATTGAACCAGGGACCTCAGGGTTA-3') together with the sequence of this region of the genome in the database revealed differences with that of the tRNA_i^{Met} sequence (20). The amplification product for *in vitro* transcription was therefore corrected in respect to the published tRNA sequence (D-loop in the published sequence was ACUGGGAGUA and the corrected sequence is AGCCUGGUA). The sequence coding for *S. acidocaldarius* tRNA_i^{Met} was thus PCR amplified using the oligonucleotides MK1 (5'-TCTGCGTAATACGACT CACTATAGGCGGCGTAGGGAAGCCTGGTATCC C-3') and MK2 (5'-TCTGCGCTGCAGTGGTGGCGGC GCCTGGATTGAACCAGGGACCTCAGGGTTA-3') as primers and oligonucleotides MK3 (5'-GGAAGCCTG GTATCCCGCAGGGCTCATAACCCTGAGGTCCCT GGTTC-3') and MK4 (5'-GAACCAGGGACCTCAGG GTTATGAGCCCTGCGGGATACCAGGCTTCC-3') as template DNA. The tRNA_i^{Met}(A9G) was amplified as described for *S. acidocaldarius* tRNA_i^{Met} but with oligonucleotide MK1' (same as MK1 but introducing the A9G mutation) instead of MK1. The sequence coding

for *T. kodakaraensis* tRNA^{Ala} was PCR amplified using oligonucleotides MK5 (5'-TCTGGAATTCTAATACG ACTCACTATAGGGCCGGTAGCTCAGCCTGGTAT G-3') and MK6 (5'-TCTGGAATTCCTGCAGTGGTGG ACCGGCCGGGATTTGAACCC-3') as primers and oligonucleotides MK7 (5'-CAGCCTGGTATGAGCGC CGCCTTGGCAAGGCGGAGGCCCGGGTTCAA TCC-3') and MK8 (5'-GGATTGAACCCGGGGCCTC CGCCTTGCCAAGGCGGCTCATAACCAGGCTG-3') as template DNA. *T. kodakaraensis* tRNA^{Asp} was PCR amplified using oligonucleotides MK9 (5'-TCTGGAATT CTAATACGACTCACTATAGCCCAGGGTGGTGTAG CCCGGCCATC-3') and MK10 (5'-TCTGGAATTCCC TGGCGCCCGGGCCGGGATTTGAACCCGG-3') as primers and oligonucleotides MK11 (5'-GTAGCCCGG CCCATCATACGGGACTGTCACTCCCCTGACCCG GGTTCAAATC-3') and MK12 (5'-GATTTGAACCCG GGTCACGGGAGTGACAGTCCCCTATGATGGGC CGGGCTAC-3') as template DNA. The DNA sequences encoding tRNA_i^{Met} and tRNA_i^{Met}A9G were cloned in the SmaI site of the pUC18 vector, giving plasmids pUC18-tRNA_i^{Met} and pUC18-tRNA_i^{Met}A9G. The DNA sequences encoding tRNA^{Ala} and tRNA^{Asp} were cloned in the EcoRI site of pUC18, giving plasmids pUC18-tRNA^{Ala} and pUC18-tRNA^{Asp}. The sequences of all the clones were checked. These plasmids allow T7 transcription of *S. acidocaldarius* tRNA_i^{Met} and tRNA_i^{Met}(A9G) and *T. kodakaraensis* tRNA^{Ala} and tRNA^{Asp}, respectively. Radioactive (³²P) *in vitro* transcripts were obtained using PstI (for *S. acidocaldarius* tRNA) or MvaI-digested plasmids (for *T. kodakaraensis* tRNA). [^α³²P]ATP and [^α³²P]GTP were purchased from Perkin Elmer. Radioactive transcripts were purified by 10% polyacrylamide gel electrophoresis.

tRNA MTase assays

The two types of tRNA MTase assays used in this work were described in (23). The first method consisted of measuring the amount of ¹⁴C transferred to total yeast tRNA (Y16243 strain), or total *E. coli* tRNA using [methyl-¹⁴C]AdoMet as the methyl donor. The reaction mixture (300 µl) consisted of 50 mM Tris-HCl pH 8, 10 mM MgCl₂, 100 µg total tRNA, 25 nCi [methyl-¹⁴C]AdoMet (50 mCi/mmol; GE Healthcare) and enzyme. The effect of TK0422p concentration on the MTase reaction was carried out using 80 µg total *E. coli* tRNA, and variable amount of TK0422p (5, 2.5, 1, 0.5 and 0.01 µg). The effect of pH on MTase reaction was measured using 50 µg *E. coli* tRNA as substrate and 5 µg enzyme. The buffers were: acetate buffer pH 4.8, MES buffer pH 5.5, phosphate buffer pH 7, HEPES buffer pH 7, CHES buffer pH 9 and CAPS buffer pH 9.75. All buffers concentrations were 50 mM. The second type of tRNA MTase assay involved *in vitro* transcribed, ³²P-labelled tRNA as substrates. Modified nucleotides were analysed by 2D thin layer chromatography (2D-TLC) on cellulose plates (Merck). First dimension was with solvent A (isobutyric acid/concentrated NH₄OH/water; 66/1/33; v/v/v); second dimension was with solvent B [0.1 M sodium phosphate pH 6.8/solid

(NH₄)₂SO₄/n-propanol; 100/60/2; v/w/v] . The nucleotides were identified using a reference map (24).

Analysis of the presence of m¹A or m¹G in *E. coli* tRNA *in vivo*

Prior to tRNA extraction, the *E. coli* strain overexpressing TK0422p and the control strain (no expression of TK0422p) were incubated for 2 h at 50°C. Then, total tRNA was extracted. An amount of 200 µg of totally hydrolysed tRNA was injected on a Supelco Discovery C18 (250 × 4.6) mm HPLC column equilibrated with ammonium acetate 0.25 M, pH 6.5. The column was eluted with a linear gradient of acetonitrile/water (40/60; v/v) at a flow rate of 1.2 ml/min. The nucleosides were detected by measuring UV absorbance at 254 nm. The standard HPLC curve was obtained by injecting 20 µl of 1 mM canonical nucleosides together with m¹A and m¹G modified nucleosides.

Localization of m¹A and m¹G in *S. acidocaldarius* tRNA_i^{Met}

The transcript of tRNA_i^{Met} or tRNA_i^{Met}(A9G) from *S. acidocaldarius* was used as substrate for the MTases TK0422p or Saci_1677p. An amount of 2 µg of tRNA was incubated in presence of 4 µg of enzyme and 0.3 mM AdoMet (Sigma) for 1 h at 50°C. As a control, transcripts were incubated in the MTase assay conditions, but without enzyme. Then the reaction was stopped by phenol extraction, transcripts were ethanol precipitated and the pellet was resuspended in 30 µl of RNase A buffer (Tris-Cl 10 mM pH 7.5, 15 mM NaCl). The resuspended solution was heated at 85°C for 5 min and then slowly cooled down to 37°C. Then 10 µg of RNase A was added and the digestion was carried out for 1 h at 70°C. Half of the RNase A digestion was 5'-end radiolabelled with 50 µCi of [³²P] ATP and 20 units of T4 polynucleotide kinase. The radiolabelled fragments were then separated by 20 or 30% polyacrylamide gel electrophoresis and revealed by autoradiography. The 8-nt long fragments (A9 or G9 at 5'-end), and 5-nt long fragments (control) were identified by their position and their intensities on the autoradiogram, excised from the gel and eluted overnight at 45°C in 200 µl water. Subsequently, they were digested by P1 nuclease and mononucleotides were separated by 2D-TLC as described in the MTase assay. The radiolabelled nucleotides present at the 5'-end of the fragments were revealed by autoradiography.

Sequence analyses

Searches of the current version of non-redundant sequence database (nr) were carried out using a local version of PSI-BLAST (25) with *E*-value threshold of 1e-5, until convergence. This threshold ensured identification of members of the Trm10 family, without paralogous members of other, more distantly related families of the SPOUT superfamily. All sequences were extracted and a multiple sequence alignment was calculated using MUSCLE (26). Structure prediction was carried out via the GeneSilico metasever (27).

RESULTS

Sulfolobus acidocaldarius Saci_1677p and *T. kodakaraensis* TK0422p are distantly related to Trm10p from *S. cerevisiae*

The tRNA_i^{Met} from *S. acidocaldarius* is the only tRNA from an hyperthermophilic archaeon sequenced to date (20). It bears an unknown modification at position 9. In yeast, the enzyme Trm10p catalyses m¹G formation at this position (21). By iterative Psi-Blast analysis, the authors identified proteins from *S. solfataricus* and *P. furiosus* which are distantly related to *S. cerevisiae* Trm10p. We used these two archaeal sequences as query for a Psi-Blast analysis of archaeal proteomes, and identified the proteins Saci_1677p from *S. acidocaldarius* (phylum Crenarchaeota) and TK0422p from *T. kodakaraensis* (phylum Euryarchaeota). These two enzymes are orthologues of *S. cerevisiae* Trm10p.

The proteins Saci_1677p from *S. acidocaldarius* and TK0422p from *T. kodakaraensis* show different tRNA MTase activities *in vitro*

Since Saci_1677p and TK0422p are distantly related to *S. cerevisiae* Trm10p, the activities of these enzymes were tested *in vitro* using unfractionated (bulk) tRNA from the *S. cerevisiae* Y16243 strain (in which the *TRM10* gene is inactivated) as substrate. The purified recombinant proteins (see 'Materials and Methods' section) were incubated at 30°C for the yeast enzyme, and at 50°C for the archaeal enzymes for an hour with [methyl-¹⁴C]AdoMet and tRNA. The choice of a reaction temperature of 50°C was based on a compromise between hyperthermophilic enzyme activity and mesophilic tRNA stability. After incubation, the tRNA was recovered by phenol extraction and ethanol precipitation and further completely hydrolysed into 5'-phosphate nucleosides by nuclease P1. The resulting hydrolysates were then analysed by 2D-TLC followed by autoradiography. The results presented in Figure 1 confirm that *S. cerevisiae* Trm10p catalyses formation of one single radioactive compound with migration characteristics identical to 1-methylguanosine (m¹G) 5'-phosphate according to reference maps (24). Interestingly, the *S. acidocaldarius* enzyme catalyses the formation of one single radioactive compound, but it corresponds to 1-methyladenosine (m¹A) 5'-phosphate. Surprisingly, the *T. kodakaraensis* TK0422p enzyme catalyses formation of two radioactive compounds, m¹A and m¹G in tRNA. The enzyme TK0422p forms approximately the same amount of m¹A and m¹G when the tRNA of the yeast strain Y16243 is used as substrate. Given that occurrence of A9 and G9 in this tRNA population is almost equal (~50% each) this result indicates that the enzyme TK0422p does not show any preference for one of these two nucleosides.

To further confirm the activities of the archaeal enzymes, the MTase activity assay was carried out as described above on unfractionated *E. coli* tRNA. The rationale behind using bulk *E. coli* tRNA arises from the fact that position 9 of *E. coli* tRNA is never modified. The

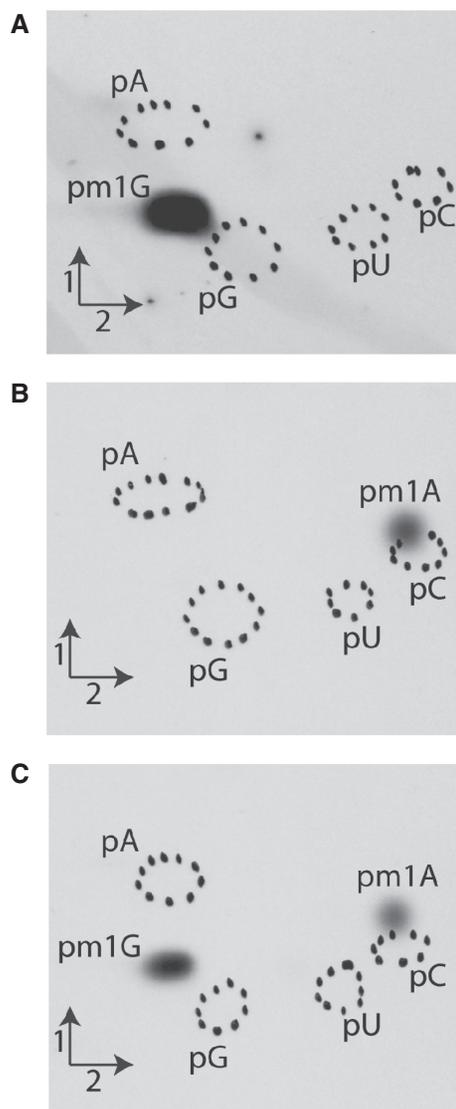


Figure 1. Analysis of MTase activities of *S. cerevisiae* Trm10p, *S. acidocaldarius* Saci_1677p and *T. kodakaraensis* TK0422p on total (bulk) tRNA from the *S. cerevisiae* Y16243 strain, in which the *TRM10* gene is inactivated. tRNA was incubated in presence of [methyl- ^{14}C]AdoMet and purified Trm10p (A), Saci_1677p (B) and TK0422p (C) as described in 'Materials and Methods' section. After incubation, tRNA was recovered and digested by nuclease P1. The resulting nucleotides were analysed by 2D-TLC and autoradiography. Circles in dotted lines show the migration of the four canonical nucleotides used as UV markers.

results shown in Figure 2 confirm those obtained using tRNA from the yeast Y16243 (*trm10::kan*) strain. Indeed, the Saci_1677p from *S. acidocaldarius* catalyses the formation of m^1A , while the TK0422p from *T. kodakaraensis* catalyses the formation of two radioactive compounds, m^1A and m^1G . The ratio $\text{m}^1\text{A}/\text{m}^1\text{G}$ is higher than what we observed using tRNA from the yeast Y16243 strain. This is consistent with the fact that there are about two times more tRNAs with A9 than with G9 in *E. coli*. Again, this confirms the absence of preference of TK0422p for one of these two nucleosides. To our knowledge this is the first description of a tRNA MTase with a broadened substrate recognition capability.

Saci_1677p catalyses m^1A formation, while TK0422p catalyses m^1A and m^1G formation on *in vitro* transcripts of archaeal tRNAs

The activity of Saci_1677p from *S. acidocaldarius* was confirmed under identical experimental conditions as above, but using [$\alpha^{32}\text{P}$]ATP-labelled tRNA substrates obtained after *in vitro* transcription by T7 RNA polymerase of synthetic *S. acidocaldarius* $\text{tRNA}_i^{\text{Met}}$ gene or $\text{tRNA}_i^{\text{Met}}\text{A9G}$ gene. After incubation, the formation of N^1 -methyladenosine was analysed as above, and the ^{32}P phosphate is only present in AMP (5'P) and AMP (5'P) derivatives. Figure 3 demonstrates unambiguously the presence of m^1A in the WT $\text{tRNA}_i^{\text{Met}}$ from *S. acidocaldarius*, showing that the enzyme is indeed a tRNA m^1A MTase. Interestingly, no m^1A was formed in a mutant of the $\text{tRNA}_i^{\text{Met}}$ where position 9 is occupied by a guanosine ($\text{tRNA}_i^{\text{Met}}\text{A9G}$), suggesting that *S. acidocaldarius* Saci_1677p acts at position 9 of tRNA, as its yeast orthologue does. Quantification of the relative amount of ^{32}P in the different radioactive spots on TLC plates revealed that about 1 mole of m^1A was formed per mole of tRNA after 1 h incubation at 50°C .

Similarly, the activity of *T. kodakaraensis* TK0422p was also confirmed using *in vitro* [$\alpha^{32}\text{P}$]ATP- and [$\alpha^{32}\text{P}$]GTP-labelled transcripts of *T. kodakaraensis* tRNA^{Ala} and tRNA^{Asp} genes. The tRNA^{Ala} contains an adenosine at position 9, while tRNA^{Asp} contains a guanosine at this position. Figure 4 shows that TK0422p catalyses formation of m^1A in the [$\alpha^{32}\text{P}$]ATP- tRNA^{Ala} (A in position 9), but not in the [$\alpha^{32}\text{P}$]ATP- tRNA^{Asp} that possesses G in position 9. Similarly, there was only formation of m^1G in the GTP-labelled tRNA^{Asp} (G9), but

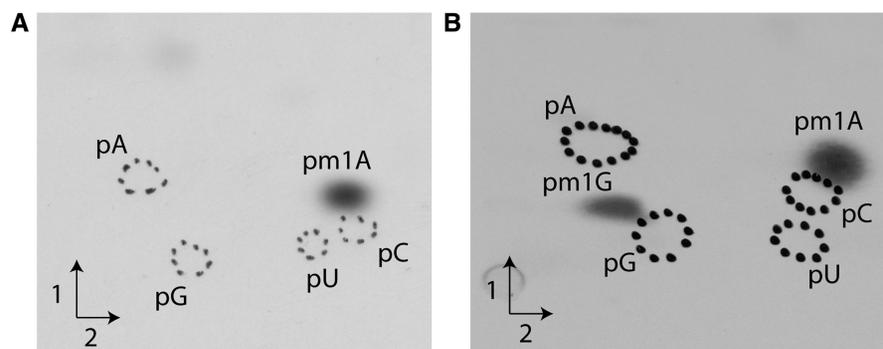


Figure 2. Analysis of MTase activities of *S. acidocaldarius* Saci_1677p and *T. kodakaraensis* TK0422p on total *E. coli* tRNA. *E. coli* tRNA was incubated in presence of 5 μg of purified Saci_1677p (A) or TK0422p (B) and [methyl- ^{14}C]AdoMet (see 'Materials and Methods' section). tRNA was recovered and digested by nuclease P1. The resulting 5'-phosphate mononucleosides were analysed by 2D-TLC followed by autoradiography.

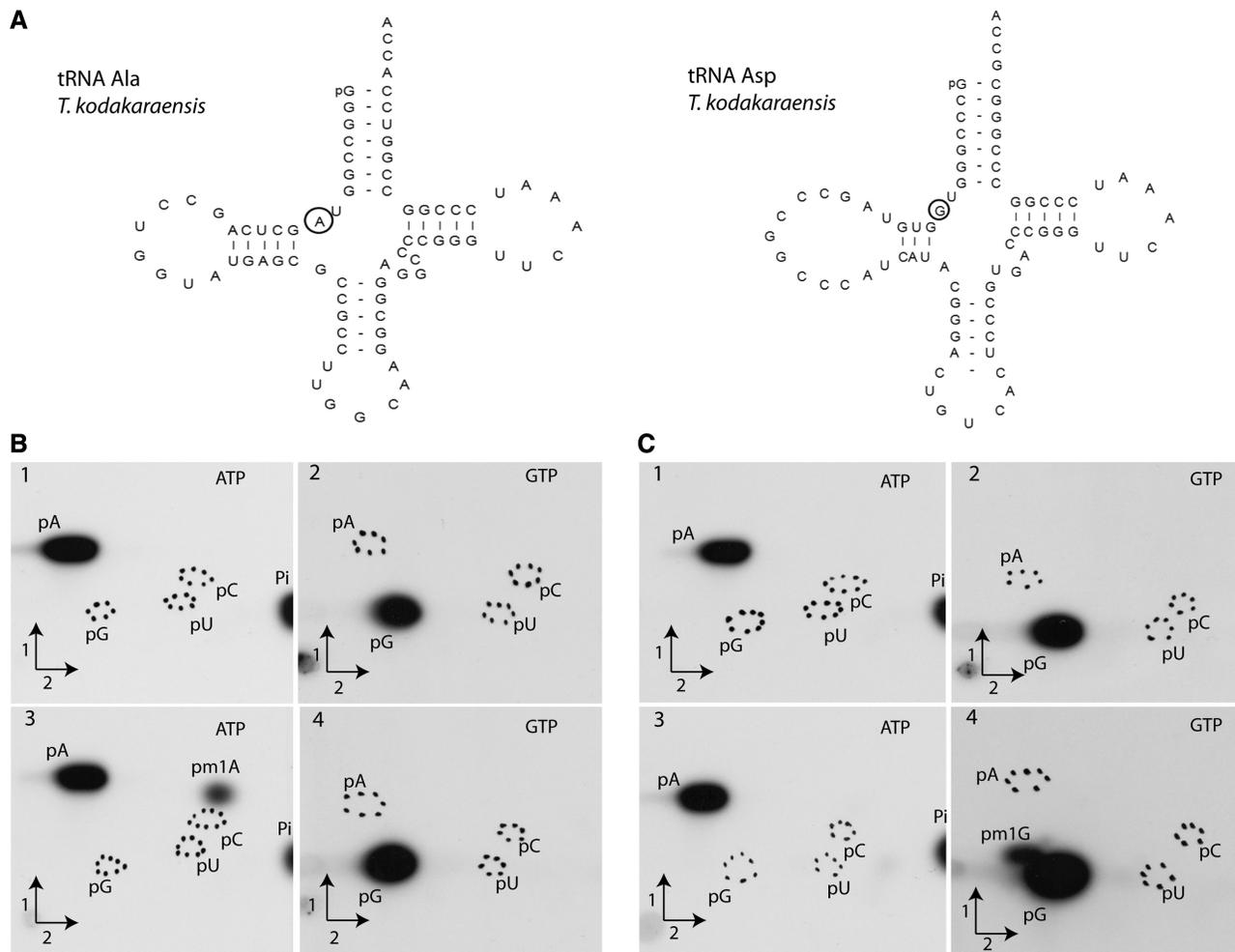


Figure 4. TK0422p from *T. kodakaraensis* methylates atom N^1 of both adenosine and guanosine of *in vitro* transcripts of *T. kodakaraensis* tRNA^{Ala} and tRNA^{Asp}. (A) Nucleotide sequence of *in vitro* transcripts of *T. kodakaraensis* tRNA^{Ala} and tRNA^{Asp}. Position 9 is circled. (B) Autoradiograms of 2D-TLC chromatograms of P1 hydrolysates of [α -³²P]ATP- or [α -³²P]GTP labelled *T. kodakaraensis* tRNA^{Ala} transcripts and (C) of *T. kodakaraensis* tRNA^{Asp} transcripts. Transcripts were incubated in presence of TK0422p for 1 h at 50°C (B3, B4, C3 and C4) or in the absence of enzyme (B1, B2, C1 and C2). Circles of dotted lines show the migration of the four canonical nucleotides used as UV markers. The radioactive nucleotide used to label the transcripts is indicated on the autoradiograms.

recombinant strain overexpressing TK0422p, m¹A could clearly be identified (Figure 6), and more m¹G was present in this tRNA preparation compared to the control strain. This result shows that TK0422p can act as a tRNA m¹A and m¹G MTase in *E. coli*.

DISCUSSION

In this work, we have identified and characterised two archaeal orthologues of Trm10p from *S. cerevisiae*. We have shown that the protein Saci_1677p from the crenarchaeon *S. acidocaldarius* catalyses N^1 methylation of an adenosine to form m¹A at position 9 of tRNA. Our data also show that Saci_1677p is specific for A9 of tRNA substrates. Interestingly, we have shown that the orthologous protein TK0422p from the euryarchaeon *T. kodakaraensis* catalyses both m¹A and m¹G formation in tRNA. We have demonstrated that both m¹A and m¹G are formed at position 9 of tRNA. To our knowledge, this

is the first description of an MTase with a broadened nucleoside recognition capability. It is interesting to point out that the protonation state of position N^1 of both adenosine and guanosine differs at physiological pH. Indeed, the N^1 atom of adenosine is not protonated at this pH, while the same position of guanosine bears a proton. This difference of protonation state raises questions about the enzymatic mechanism of TK0422p. In this article, we have shown that the pH of the methylation reaction has an influence on the efficacy of m¹A or m¹G formation. Indeed, the relative efficiency of m¹G formation by TK0422p increases with increasing pH, especially at pH values above 9.5 which corresponds to the pK_a of N^1 of G (28). This could reflect the need of this enzyme to deprotonate G to be able to catalyse the methyl transfer, although other possibilities are not excluded, such as an influence of pH on tRNA or enzyme structure.

Figure 7 illustrates sequence conservation between Trm10p from yeast and the two archaeal proteins

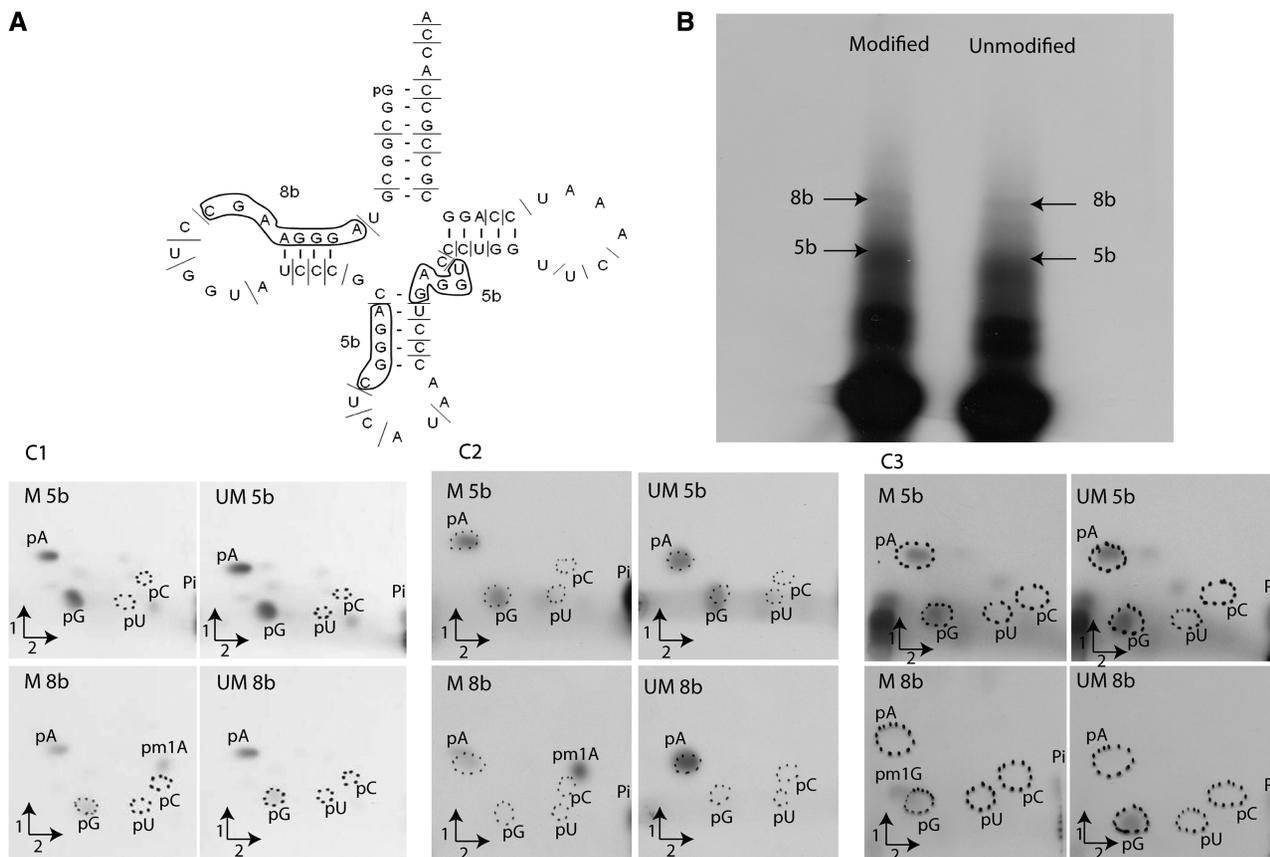


Figure 5. Localisation of m^1A and m^1G modifications in *S. acidocaldarius* $tRNA_i^{Met}$ and $tRNA_i^{Met}A9G$. (A) RNase A digestion profile of *S. acidocaldarius* $tRNA_i^{Met}$. The 8-nt long fragments (8b) and the 5-nt long fragments (5b) are boxed. (B) Autoradiogram of the polyacrylamide gel used to separate the RNase A fragments of the modified and unmodified $tRNA_i^{Met}$ transcripts. The 8-nt long fragments (8b) and the 5-nt long fragments (5b) are shown by arrows. (C) The 8-nt long fragments and the 5-nt long fragments obtained from transcripts of $tRNA_i^{Met}$ (panels C1 and C2) or $tRNA_i^{Met}A9G$ (panel C3) incubated in the presence or absence of Saci_1677p (panel C1) or TK0422p (panels C2 and C3) were hydrolysed by nuclease P1. The nucleotides in the hydrolysates were separated by 2D-TLC. The nature of the nucleotide at the 5' end of the fragments was revealed by autoradiography. M is for the transcripts enzymatically modified and UM for those left unmodified.

Table 1. pH dependence of m^1A and m^1G formation by TK0422p from *T. kodakaraensis*

pH	m^1G/m^1A ratio
4.8	0
5.5	0.06
7	0.42
9	0.18
9.75	1.43

The MTase activity was measured using total (bulk) *E. coli* tRNA as substrate. tRNA was incubated in presence of [methyl- ^{14}C]AdoMet and purified TK0422p protein. The different buffers are described in 'Materials and Methods' section. After incubation, tRNA was recovered and the formation of m^1G and m^1A was measured as described in 'Materials and Methods' section.

analysed in this work. According to structure prediction methods, the catalytic core of the SPOUT domain spans residues 100–260 of TK0422p (and the corresponding positions in the homologous sequences), and includes five

β -strands and six α -helices. The N-terminus is conserved only between the archaeal proteins, but not with the eukaryotic protein. Due to uncertain alignments with known SPOUT structures we were unable to generate a confident 3D model of the catalytic domain, nonetheless the mapping of clusters of conserved residues on predicted secondary structures suggests that the active site is composed of nearly invariant (on the level of the whole family) residues D104, Q122 and D206 (numbering for TK0422p). Interestingly, there appears to be no equivalent catalytic residues between the Trm10p family and the bacterial TrmD family of m^1G MTases, also members of the SPOUT superfamily that act on the position G37 in tRNA (29). This suggests that the N^1 purine methylation activity has evolved independently at least two times in the SPOUT superfamily. Independent origin of the N^1 purine methylation activity has been also postulated for MTases of the RFM superfamily, i.e. tRNA: m^1A58 MTase TrmI, tRNA: m^1A22 MTase TrmK, and 16S rRNA: m^1A1408 MTase KamB, which also present different active sites despite the common fold of the catalytic domain (30,31). This variety of protein folds and active sites available to carry out the same type of reaction

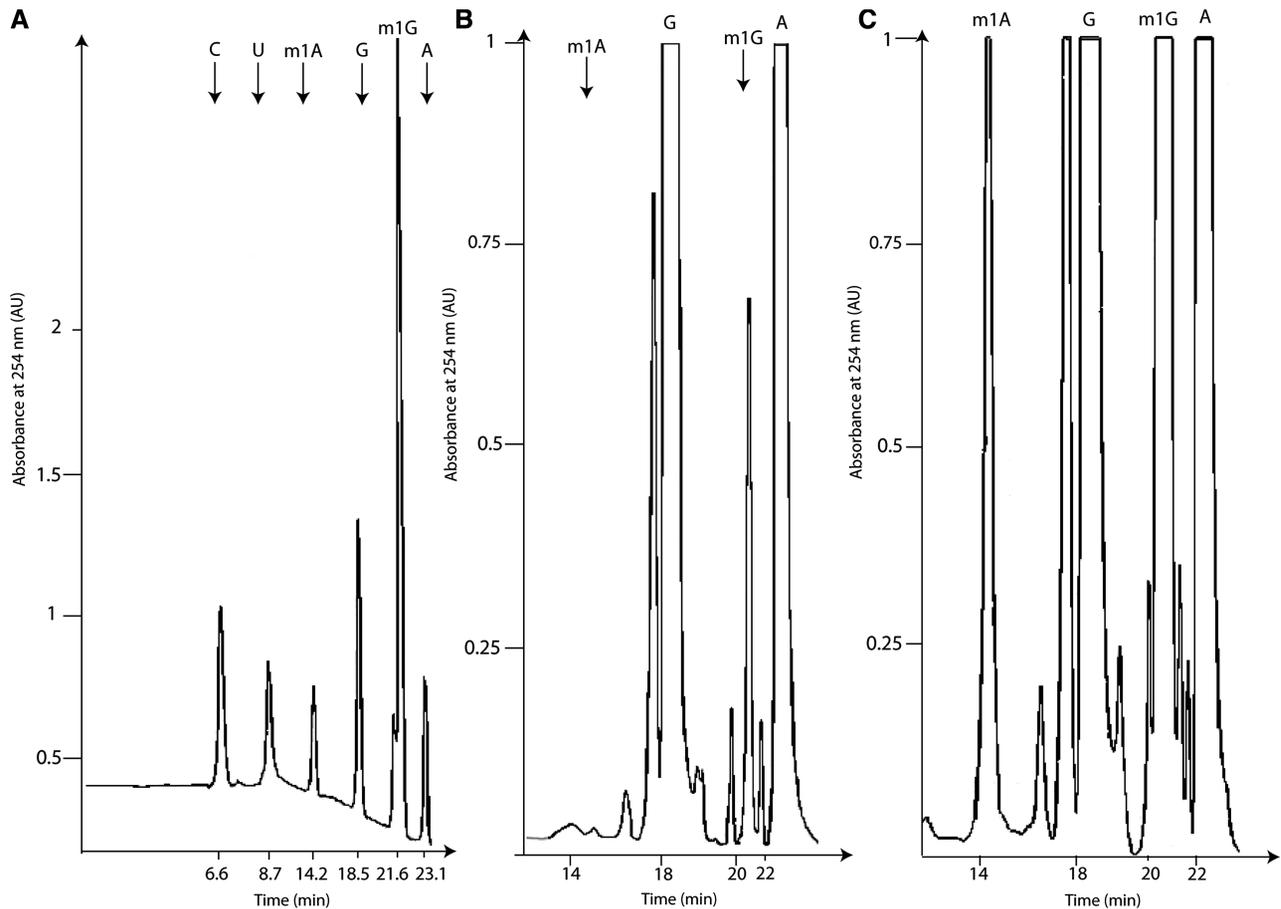


Figure 6. *Thermococcus kodakarensis* TK0422p MTase displays tRNA (m¹A and m¹G) MTase activity in *E. coli* *in vivo*. tRNA from the *E. coli* strain expressing (C) or not (B) TK0422p were extracted and hydrolysed by nuclease P1, snake venom phosphodiesterase and alkaline phosphatase, and then analysed by HPLC. The peaks corresponding to m¹A and m¹G are indicated by arrows. A standard curve with the reference nucleosides is given in (A).

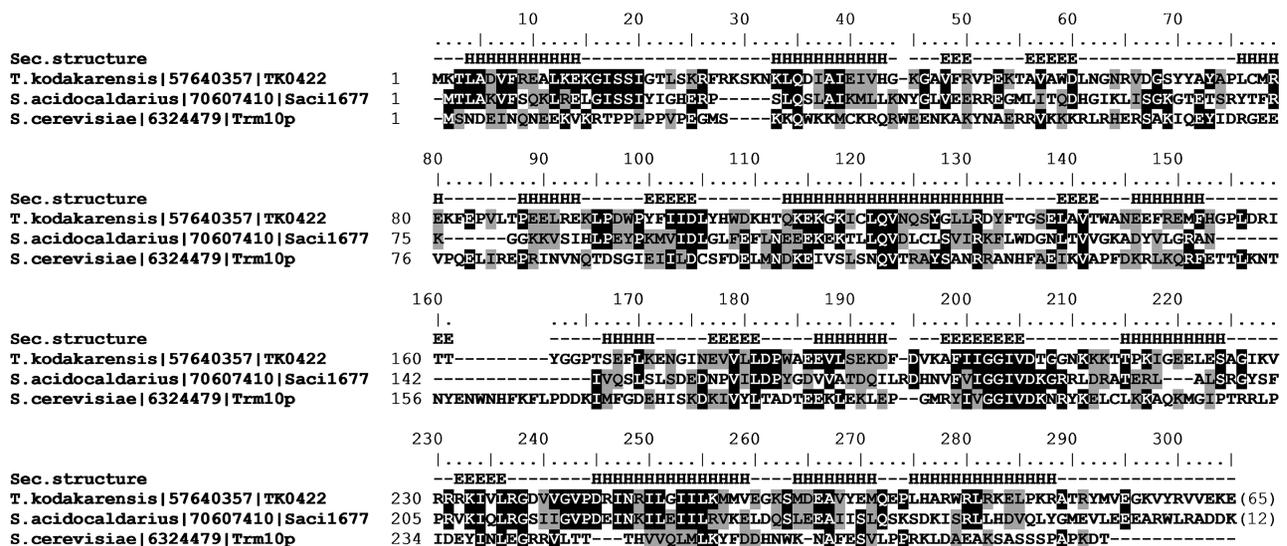


Figure 7. Alignment of three experimentally characterised members of the Trm10p family, including the eukaryotic founding member of this family and two archaeal proteins analysed in this work. Residues that are conserved and physicochemically similar in >50% of the sequences are indicated by black and grey shading, respectively. Secondary structures predicted for TK0422p are indicated as E (extended) and H (helix).

suggests that N^1 purine methylation is probably relatively easy for an enzyme to evolve (e.g. from an MTase of a different specificity).

Unfortunately, we were unable to identify a negatively charged residue conserved between TK0422p (m^1G and m^1A MTase) and Trm10p (m^1G MTase) but absent from Saci_1677p (m^1A MTase) that could explain the inability of the latter protein to deprotonate and methylate guanosine. Therefore, the molecular basis of the different specificities in the Trm10p family remains a mystery. This problem may be approached in the future by experimental determination of a high-resolution structure for one of the family members, characterisation of specificities of numerous additional members of the family, or by mutagenesis of individual members. In particular the availability of a crystal structure for a Trm10p family member would enable its comparison with the known structures of evolutionarily related TrmD MTases and would help to evaluate the hypothesis of convergent evolution of their active sites for an analogous reaction, upon homologous protein scaffold.

Interestingly, the distribution of Trm10p orthologues in Archaea is restricted to hyperthermophiles. We found single representatives of this family in Crenarchaeota (*S. acidocaldarius*, *S. tokodaii*, *S. solfataricus*, *S. islandicus*, *Hyperthermus butylicus*, *Ignicoccus hospitalis*, *Aeropyrum pernix*, *Pyrobaculum aerophilum*, *P. arsenaticum*, *P. calidifontis*, *P. islandicum*, *Thermoproteus neutrophilus*, *Caldivirga maquilingensis*, *Metallosphaera sedula*) and in Euryarchaeota (*T. kodakaraensis*, *T. gammatolerans*, *T. omurineus*, *T. barophilus*, *T. sibiricus*, *T. sp. AM4*, *Archaeoglobus fulgidus*, *Methanopyrus kandleri*, *Pyrococcus furiosus*, *P. abyssi* and *P. horikoshii*), as well as in Nanoarchaeum *equitans*. On the other hand, Trm10p is absent from the mesophilic archaeon *Halobacterium volcanii*, which is known to lack m^1A or m^1G at position 9 (32). This suggests that m^1G or m^1A modification may contribute to the thermostability of archaeal tRNAs.

A stabilizing function of base methylation has been recently identified for the m^7G46 modification in a thermophilic bacterium *T. thermophilus* (33). In tRNA crystal structures the base A9 is stacked between bases 45 and 46. Modelling of the *S. acidocaldarius* tRNA with and without modifications (data not shown) suggests that the methyl group of m^7G46 would be located only about 5–6 Å from the methyl group of m^1A9 . However, G46 is not methylated in Archaea due to the absence of the TrmB family MTase responsible for this activity in Bacteria and Eukaryota (34). The methyl group on residue A9 may fill a cavity between bases 45 and 46 and the backbone of residue 22. This could increase the surface of interaction between this residue and G46, which may contribute to the increased stability of the tRNA molecule. Furthermore, the positive charge on m^1A may have a stabilisatory function due to electrostatic interactions with the neighbouring phosphate groups of residues 22 and 23. Thus, it is tempting to speculate that m^1A9 may fulfil a similar stabilisatory role in thermophilic Archaea as m^7G46 does in thermophilic bacteria.

ACKNOWLEDGEMENTS

The authors warmly acknowledge D. Gigot (ULB, Belgium) for help and advice during protein purifications and HPLC analyses. We are grateful to D. Charlier (VUB, Belgium), H. Grosjean (CNRS, France) and T.J. Santangelo (Ohio State University, USA) for the gift of archaeal genomic DNAs. J.M.B. thanks Tomasz Puton (Adam Mickiewicz University, Poznan, Poland) and Irina Tuszynska (IIMCB, Warsaw, Poland) for their help with tRNA modelling and structural analysis.

FUNDING

Fonds pour le Recherche Fondamentale Collective [grant number 2.4.520.05F] and by the Fonds D. et A. Van Buuren; Fonds pour la Formation à la Recherche dans l'Industrie et dans l'Agriculture fellowship (to M.K.); EURASNET Network of Excellence grant in the 6th Framework Program of the European Commission and by the Polish Ministry of Science and Higher Education [grant number 301 2396 33] (to J.M.B.); Polish Ministry of Science and Higher Education [grant number 301 105 32/3599] and by the START fellowship from the Foundation for Polish Science (to K.L.T.). Funding for open access charge: Fonds pour la Recherche Fondamentale Collective.

Conflict of interest statement. None declared.

REFERENCES

- Jühling, F., Mörl, M., Hartmann, R.K., Sprinzl, M., Stadler, P.F. and Pütz, J. (2009) tRNAdb 2009: compilation of tRNA sequences and tRNA genes. *Nucleic Acids Res.*, **37**, D159–D162.
- Czerwoniec, A., Dunin-Horkawicz, S., Purta, E., Kaminska, K.H., Kasprzak, J.M., Bujnicki, J.M., Grosjean, H. and Rother, K. (2009) MODOMICS: a database of RNA modification pathways 2008 update. *Nucleic Acids Res.*, **37**, D118–D121.
- Urbonavicius, J., Skouloubris, S., Myllykallio, H. and Grosjean, H. (2005) Identification of a novel gene encoding a flavin-dependent tRNA: m^5U methyltransferase in bacteria-evolutionary implications. *Nucleic Acids Res.*, **33**, 3955–3964.
- Schubert, H.L., Blumenthal, R.M. and Cheng, X. (2003) Many paths to methyltransfer: a chronicle of convergence. *Trends Biochem. Sci.*, **28**, 329–335.
- Kozbial, P.Z. and Mushegian, A.R. (2005) Natural history of S-adenosylmethionine-binding proteins. *BMC Struct. Biol.*, **5**, 19.
- Kaminska, K.H., Purta, E., Hansen, L.H., Bujnicki, J.M., Vester, B. and Long, K.S. (2009) Insights into the structure, function and evolution of the radical-SAM 23S rRNA methyltransferase Cfr that confers antibiotic resistance in bacteria. *Nucleic Acids Res.*, **38**, 1652–1663.
- Anantharaman, V., Koonin, E.V. and Aravind, L. (2002) SPOUT: a class of methyltransferases that includes SpoU and TrmD RNA methylase superfamilies novel superfamilies of predicted prokaryotic RNA methylases. *J. Mol. Microbiol. Biotechnol.*, **4**, 71–75.
- Tkaczuk, K.L., Dunin-Horkawicz, S., Purta, E. and Bujnicki, J.M. (2007) Structural and evolutionary bioinformatics of the SPOUT superfamily of methyltransferases. *BMC Bioinformatics*, **8**, 73–103.
- Renalier, M.H., Joseph, N., Gaspin, C., Thebault, P. and Mougou, A. (2005) The Cm56 tRNA modification in Archaea is catalyzed either by a specific 2'-O-methylase, or a C/D sRNP. *RNA*, **11**, 1051–1063.
- Kuratani, M., Bessho, Y., Nishimoto, M., Grosjean, H. and Yokoyama, S. (2008) Crystal structure and mutational study of a

- unique SpoU family archaeal methylase that forms 2'-O-methylcytidine at position 56 of tRNA. *J. Mol. Biol.*, **375**, 1064–1075.
11. Armengaud, J., Urbonavicius, J., Fernandez, B., Chaussinand, G., Bujnicki, J.M. and Grosjean, H. (2004) N^2 -methylation of guanosine at position 10 in tRNA is catalyzed by a THUMP domain-containing, S-adenosylmethionine-dependent methyltransferase, conserved in Archaea and Eukaryota. *J. Biol. Chem.*, **279**, 37142–37152.
 12. Urbonavicius, J., Armengaud, J. and Grosjean, H. (2006) Identity elements required for enzymatic formation of N^2 , N^2 -dimethylguanosine from N^2 -monomethylated derivative and its possible role in avoiding alternative conformations in archaeal tRNA. *J. Mol. Biol.*, **357**, 387–399.
 13. Constantinesco, F., Motorin, Y. and Grosjean, H. (1999) Characterization and enzymatic properties of tRNA (guanine 26, N^2 , N^2 -dimethyltransferase (Trm1p) from *Pyrococcus furiosus*. *J. Mol. Biol.*, **291**, 375–392.
 14. Ihsanawati, N., Nishimoto, M., Higashijima, K., Shirouzu, M., Grosjean, H., Bessho, Y. and Yokoyama, S. (2008) Crystal structure of tRNA N^2 , N^2 -guanosine dimethyltransferase Trm1 from *Pyrococcus horikoshii*. *J. Mol. Biol.*, **383**, 871–884.
 15. Auxilien, S., El Khadali, F., Rasmussen, A., Douthwaite, S. and Grosjean, H. (2007) Archaease from *Pyrococcus abyssi* improves substrate specificity and solubility of a tRNA m^7C methyltransferase. *J. Biol. Chem.*, **282**, 18711–18721.
 16. Christian, T., Evilia, C., Williams, S. and Hou, Y.-M. (2004) Distinct origins of tRNA(m^1G37) methyltransferase. *J. Mol. Biol.*, **339**, 707–719.
 17. Björk, G.R., Jacobsson, K., Nilsson, K., Johansson, M.J., Byström, A.S. and Persson, O.P. (2001) A primordial tRNA modification required for the evolution of life? *EMBO J.*, **20**, 231–239.
 18. Walbott, H., Leulliot, N., Grosjean, H. and Golinelli-Pimpaneau, B. (2008) The crystal structure of *Pyrococcus abyssi* tRNA (uracil-54, C5)-methyltransferase provides insights into its tRNA specificity. *Nucleic Acids Res.*, **36**, 4929–4940.
 19. Roovers, M., Wouters, J., Bujnicki, J., Tricot, C., Stalon, V., Grosjean, H. and Droogmans, L. (2004) A primordial RNA modification enzyme: the case of tRNA (m^1A) methyltransferase. *Nucleic Acids Res.*, **32**, 465–476.
 20. Kuchino, Y., Ihara, M., Yabusaki, Y. and Nishimura, S. (1982) Initiator tRNAs from archaeobacteria show common unique sequence characteristics. *Nature*, **298**, 684–685.
 21. Jackman, J.E., Montange, R.K., Malik, H.S. and Phizicky, E.M. (2003) Identification of the yeast gene encoding the tRNA m^1G methyltransferase responsible for modification at position 9. *RNA*, **9**, 574–585.
 22. Reyes, V.M. and Abelson, J. (1987) A synthetic substrate for tRNA splicing. *Anal. Biochem.*, **166**, 90–106.
 23. Droogmans, L., Roovers, M., Bujnicki, J.M., Tricot, C., Hartsch, T., Stalon, V. and Grosjean, H. (2003) Cloning and characterization of tRNA (m^1A58) methyltransferase (TrmI) from *Thermus thermophilus* HB27, a protein required for cell growth at extreme temperatures. *Nucleic Acids Res.*, **31**, 2148–2156.
 24. Grosjean, H., Keith, G. and Droogmans, L. (2004) Detection and quantification of modified nucleotides in RNA using thin-layer chromatography. *Methods Mol. Biol.*, **265**, 357–391.
 25. Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W. and Lipman, D.J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.*, **25**, 3389–3402.
 26. Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.*, **32**, 1792–1797.
 27. Kurowski, M.A. and Bujnicki, J.M. (2003) GeneSilico protein structure prediction meta-server. *Nucleic Acids Res.*, **31**, 3305–3307.
 28. Rogstad, K., Jang, Y., Sowers, L. and Goddard, W. (2003) First principles calculations of the pKa values and tautomers of isoguanine and xanthine. *Chem. Res. Toxicol.*, **16**, 1455–1462.
 29. Elkins, P.A., Watts, J.M., Zalacain, M., van Thiel, A., Vitazka, P.R., Redlak, M., Andraos-Selim, C., Rastinejad, F. and Holmes, W.M. (2003) Insights into catalysis by a knotted TrmD tRNA methyltransferase. *J. Mol. Biol.*, **333**, 931–949.
 30. Roovers, M., Kaminska, K.H., Tkaczuk, K.L., Gigot, D., Droogmans, L. and Bujnicki, J.M. (2008) The YqfN protein of *Bacillus subtilis* is the tRNA: m^1A22 methyltransferase (TrmK). *Nucleic Acids Res.*, **36**, 3252–3262.
 31. Kosciński, L., Feder, M. and Bujnicki, J.M. (2007) Identification of a missing sequence and functionally important residues of 16S rRNA: m^1A1408 methyltransferase KamB that causes bacterial resistance to aminoglycoside antibiotics. *Cell Cycle*, **6**, 1268–1271.
 32. Gupta, R. (1984) *Halobacterium volcanii* tRNAs. Identification of 41 tRNAs covering all amino acids, and the sequences of 33 class I tRNAs. *J. Biol. Chem.*, **259**, 9461–9471.
 33. Tomikawa, C., Yokogawa, T., Kanai, T. and Hori, H. (2010) N^7 -methylguanine at position 46 (m^7G46) in tRNA from *Thermus thermophilus* is required for cell viability at high temperatures through a tRNA modification network. *Nucleic Acids Res.*, **38**, 942–957.
 34. Purta, E., van Vliet, F., Tricot, C., De Bie, L.G., Feder, M., Skowronek, K., Droogmans, L. and Bujnicki, J.M. (2005) Sequence-structure-function relationships of a tRNA (m^7G46) methyltransferase studied by homology modeling and site-directed mutagenesis. *Proteins*, **59**, 482–488.